

	215	220	225
	Pro Pro Arg Glu Val Val Pro Arg Pro Arg Pro Gly Val Thr Glu		
	230	235	240
	Ala Thr Ile Thr Gly Leu Glu Pro Gly Thr Glu Tyr Thr Ile Tyr		
5	245	250	255
	Val Ile Ala Leu Lys Asn Asn Gln Lys Ser Glu Pro Leu Ile Gly		
	260	265	270
	Arg Lys Lys Thr Ser Ala Ile Pro Ala Pro Thr Asp Leu Lys Phe		
	275	280	285
10	Thr Gln Val Thr Pro Thr Ser Leu Ser Ala Gln Trp Thr Pro Pro		
	290	295	300
	Asn Val Gln Leu Thr Gly Tyr Arg Val Arg Val Thr Pro Lys Glu		
	305	310	315
	Lys Thr Gly Pro Met Lys Glu Ile Asn Leu Ala Pro Asp Ser Ser		
15	320	325	330
	Ser Val Val Val Ser Gly Leu Met Val Ala Thr Lys Tyr Glu Val		
	335	340	345
	Ser Val Tyr Ala Leu Lys Asp Thr Leu Thr Ser Arg Pro Ala Gln		
	350	355	360
20	Gly Val Val Thr Thr Leu Glu Asn Val Ser Pro Pro Arg Arg Ala		
	365	370	375
	Arg Val Thr Asp Ala Thr Glu Thr Thr Ile Thr Ile Ser Trp Arg		
	380	385	390
	Thr Lys Thr Glu Thr Ile Thr Gly Phe Gln Val Asp Ala Val Pro		
25	395	400	405

Ala Asn Gly Gln Thr Pro Ile Gln Arg Thr Ile Lys Pro Asp Val		
	410	420
Arg Ser Tyr Thr Ile Thr Gly Leu Gln Pro Gly Thr Asp Tyr Lys		
	425	435
Ile Tyr Leu Tyr Thr Leu Asn Asp Asn Ala Arg Ser Ser Pro Val		
	440	450
Val Ile Asp Ala Ser Thr Ala Ile Asp Ala Pro Ser Asn Leu Arg		
	455	465
Phe Leu Ala Thr Thr Pro Asn Ser Leu Leu Val Ser Trp Gln Pro		
	470	480
Pro Arg Ala Arg Ile Thr Gly Tyr Ile Ile Lys Tyr Glu Lys Pro		
	485	495
Gly Ser Pro Pro Arg Glu Val Val Pro Arg Pro Arg Pro Gly Val		
	500	510
Thr Glu Ala Thr Ile Thr Gly Leu Glu Pro Gly Thr Glu Tyr Thr		
	515	525
Ile Tyr Val Ile Ala Leu Lys Asn Asn Gln Lys Ser Glu Pro Leu		
	530	540
Ile Gly Arg Lys Lys Thr Ser		
	545	

SEQ. ID No. 14

LENGTH: 826

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULAR TYPE: peptide

SEQUENCE:

Ala	Ala	Ser	Pro	Thr	Asp	Leu	Arg	Phe	Thr	Asn	Ile	Gly	Pro	Asp
				5					10					15
Thr	Met	Arg	Val	Thr	Trp	Ala	Pro	Pro	Pro	Ser	Ile	Asp	Leu	Thr
				20					25					30
Asn	Phe	Leu	Val	Arg	Tyr	Ser	Pro	Val	Lys	Asn	Glu	Glu	Asp	Val
				35					40					45
Ala	Glu	Leu	Ser	Ile	Ser	Pro	Ser	Asp	Asn	Ala	Val	Val	Leu	Thr
				50					55					60
Asn	Leu	Leu	Pro	Gly	Thr	Glu	Tyr	Val	Val	Ser	Val	Ser	Ser	Val
				65					70					75
Tyr	Glu	Gln	His	Glu	Ser	Thr	Pro	Leu	Arg	Gly	Arg	Gln	Lys	Thr
				80					85					90
Gly	Leu	Asp	Ser	Pro	Thr	Gly	Ile	Asp	Phe	Ser	Asp	Ile	Thr	Ala
				95					100					105
Asn	Ser	Phe	Thr	Val	His	Trp	Ile	Ala	Pro	Arg	Ala	Thr	Ile	Thr
				110					115					120
Gly	Tyr	Arg	Ile	Arg	His	His	Pro	Glu	His	Phe	Ser	Gly	Arg	Pro
				125					130					135
Arg	Glu	Asp	Arg	Val	Pro	His	Ser	Arg	Asn	Ser	Ile	Thr	Leu	Thr
				140					145					150
Asn	Leu	Thr	Pro	Gly	Thr	Glu	Tyr	Val	Val	Ser	Ile	Val	Ala	Leu
				155					160					165

	Asn Gly Arg Glu Glu Ser Pro Leu Leu Ile Gly Gln Gln Ser Thr	
	170	175 180
	Val Ser Asp Val Pro Arg Asp Leu Glu Val Val Ala Ala Thr Pro	
	185	190 195
5	Thr Ser Leu Leu Ile Ser Trp Asp Ala Pro Ala Val Thr Val Arg	
	200	205 210
	Tyr Tyr Arg Ile Thr Tyr Gly Glu Thr Gly Gly Asn Ser Pro Val	
	215	220 225
	Gln Glu Phe Thr Val Pro Gly Ser Lys Ser Thr Ala Thr Ile Ser	
10	230	235 240
	Gly Leu Lys Pro Gly Val Asp Tyr Thr Ile Thr Val Tyr Ala Val	
	245	250 255
	Thr Gly Arg Gly Asp Ser Pro Ala Ser Ser Lys Pro Ile Ser Ile	
	260	265 270
15	Asn Tyr Arg Thr Glu Ile Asp Lys Pro Ser Thr Ser Ala Ile Pro	
	275	280 285
	Ala Pro Thr Asp Leu Lys Phe Thr Gln Val Thr Pro Thr Ser Leu	
	290	295 300
	Ser Ala Gln Trp Thr Pro Pro Asn Val Gln Leu Thr Gly Tyr Arg	
20	305	310 315
	Val Arg Val Thr Pro Lys Glu Lys Thr Gly Pro Met Lys Glu Ile	
	320	325 330
	Asn Leu Ala Pro Asp Ser Ser Ser Val Val Val Ser Gly Leu Met	
	335	340 345
25	Val Ala Thr Lys Tyr Glu Val Ser Val Tyr Ala Leu Lys Asp Thr	

	350	355	360
	Leu Thr Ser Arg Pro Ala Gln Gly Val Val Thr Thr Leu Glu Asn		
	365	370	375
	Val Ser Pro Pro Arg Arg Ala Arg Val Thr Asp Ala Thr Glu Thr		
5	380	385	390
	Thr Ile Thr Ile Ser Trp Arg Thr Lys Thr Glu Thr Ile Thr Gly		
	395	400	405
	Phe Gln Val Asp Ala Val Pro Ala Asn Gly Gln Thr Pro Ile Gln		
	410	415	420
10	Arg Thr Ile Lys Pro Asp Val Arg Ser Tyr Thr Ile Thr Gly Leu		
	425	430	435
	Gln Pro Gly Thr Asp Tyr Lys Ile Tyr Leu Tyr Thr Leu Asn Asp		
	440	445	450
	Asn Ala Arg Ser Ser Pro Val Val Ile Asp Ala Ser Thr Ala Ile		
15	455	460	465
	Asp Ala Pro Ser Asn Leu Arg Phe Leu Ala Thr Thr Pro Asn Ser		
	470	475	480
	Leu Leu Val Ser Trp Gln Pro Pro Arg Ala Arg Ile Thr Gly Tyr		
	485	490	495
20	Ile Ile Lys Tyr Glu Lys Pro Gly Ser Pro Pro Arg Glu Val Val		
	500	505	510
	Pro Arg Pro Arg Pro Gly Val Thr Glu Ala Thr Ile Thr Gly Leu		
	515	520	525
	Glu Pro Gly Thr Glu Tyr Thr Ile Tyr Val Ile Ala Leu Lys Asn		
25	530	535	540

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Asn	Gln	Lys	Ser	Glu	Pro	Leu	Ile	Gly	Arg	Lys	Lys	Thr	Ser	Ala
				545					550					555
Ile	Pro	Ala	Pro	Thr	Asp	Leu	Lys	Phe	Thr	Gln	Val	Thr	Pro	Thr
				560					565					570
Ser	Leu	Ser	Ala	Gln	Trp	Thr	Pro	Pro	Asn	Val	Gln	Leu	Thr	Gly
				575					580					585
Tyr	Arg	Val	Arg	Val	Thr	Pro	Lys	Glu	Lys	Thr	Gly	Pro	Met	Lys
				590					595					600
Glu	Ile	Asn	Leu	Ala	Pro	Asp	Ser	Ser	Ser	Val	Val	Val	Ser	Gly
				605					610					615
Leu	Met	Val	Ala	Thr	Lys	Tyr	Glu	Val	Ser	Val	Tyr	Ala	Leu	Lys
				620					625					630
Asp	Thr	Leu	Thr	Ser	Arg	Pro	Ala	Gln	Gly	Val	Val	Thr	Thr	Leu
				635					640					645
Glu	Asn	Val	Ser	Pro	Pro	Arg	Arg	Ala	Arg	Val	Thr	Asp	Ala	Thr
				650					655					660
Glu	Thr	Thr	Ile	Thr	Ile	Ser	Trp	Arg	Thr	Lys	Thr	Glu	Thr	Ile
				665					670					675
Thr	Gly	Phe	Gln	Val	Asp	Ala	Val	Pro	Ala	Asn	Gly	Gln	Thr	Pro
				680					685					690
Ile	Gln	Arg	Thr	Ile	Lys	Pro	Asp	Val	Arg	Ser	Tyr	Thr	Ile	Thr
				695					700					705
Gly	Leu	Gln	Pro	Gly	Thr	Asp	Tyr	Lys	Ile	Tyr	Leu	Tyr	Thr	Leu
				710					715					720
Asn	Asp	Asn	Ala	Arg	Ser	Ser	Pro	Val	Val	Ile	Asp	Ala	Ser	Thr

	725	730	735
Ala Ile Asp Ala Pro Ser Asn Leu Arg Phe Leu Ala Thr Thr Pro			
	740	745	750
Asn Ser Leu Leu Val Ser Trp Gln Pro Pro Arg Ala Arg Ile Thr			
	755	760	765
Gly Tyr Ile Ile Lys Tyr Glu Lys Pro Gly Ser Pro Pro Arg Glu			
	770	775	780
Val Val Pro Arg Pro Arg Pro Gly Val Thr Glu Ala Thr Ile Thr			
	785	790	795
Gly Leu Glu Pro Gly Thr Glu Tyr Thr Ile Tyr Val Ile Ala Leu			
	800	805	810
Lys Asn Asn Gln Lys Ser Glu Pro Leu Ile Gly Arg Lys Lys Thr			
	815	820	825
Ser			

SEQ. ID No. 15

LENGTH: 38

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULAR TYPE: other nucleic acid (synthetic DNA)

SEQUENCE:

AAACCATGGC AGCTAGCGCT ATTCCTGCAC CAACTGAC

38

SEQ. ID No. 16

LENGTH: 36

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULAR TYPE: other nucleic acid (synthetic DNA)

SEQUENCE:

AAAGGATCCC TAACTAGTCT TTTTCCTTCC AATCAG

36

SEQ. ID No. 17

LENGTH: 1644

TYPE: nucleic acid

STRANDEDNESS: double

TOPOLOGY: linear

MOLECULAR TYPE: other nucleic acid (DNA encoding an
artificial polypeptide)

SEQUENCE:

ATGGCAGCTA GCGCTATTCC TGCACCAACT GACCTGAAGT TCACTCAGGT CACACCCACA 60
AGCGTGAGCG CCCAGTGGAC ACCACCCAAT GTTCAGCTCA CTGGATATCG AGTGCGGGTG 120
ACCCCCAAGG AGAAGACCGG ACCAATGAAA GAAATCAACC TTGCTCCTGA CAGCTCATCC 180
GTGGTTGTAT CAGGACTTAT GGTGGCCACC AAATATGAAG TGAGTGTCTA TGCTCTTAAG 240
GACACTTTGA CAAGCAGACC AGCTCAGGGT GTTGTCACCA CTCTGGAGAA TGTGAGCCCA 300
CCAAGAAGGG CTCGTGTGAC AGATGCTACT GAGACCACCA TCACCATTAG CTGGAAGAACC 360
AAGACTGAGA CGATCACTGG CTTCCAAGTT GATGCCGTTT CAGCCAATGG CCAGACTCCA 420
ATCCAGAGAA CCATCAAGCC AGATGTCAGA AGCTACACCA TCACAGGTTT ACAACCAGGC 480
ACTGACTACA AGATCTACCT GTACACCTTG AATGACAATG CTCGGAGCTC CCCTGTGGTC 540

ATCGACGCCT CCACTGCCAT TGATGCACCA TCCAACCTGC GTTTCCTGGC CACCACACCC 600
AATTCCCTTGC TGGTATCATG GCAGCCGCCA CGTGCCAGGA TTACCGGCTA CATCATCAAG 660
TATGAGAAGC CTGGGTCTCC TCCCAGAGAA GTGGTCCCTC GGCCCCGCC TGGTGTACACA 720
GAGGCTACTA TTA CTGGCCT GGAACCGGA ACCGAATATA CAATTTATGT CATTGCCCTG 780
5 AAGAATAATC AGAAGAGCGA GCCCCTGATT GGAAGGAAAA AGACTAGCGC TATTCTTGCA 840
CCAACTGACC TGAAGTTCAC TCAGGTCACA CCCACAAGCC TGAGCGCCCA GTGGACACCA 900
CCCAATGTTC AGCTCACTGG ATATCGAGTG CGGGTGACCC CCAAGGAGAA GACCGGACCA 960
ATGAAAGAAA TCAACCTTGC TCCTGACAGC TCATCCGTGG TTGTATCAGG ACTTATGGTG 1020
GCCACCAAAT ATGAAGTGAG TGTCTATGCT CTTAAGGACA CTTTGACAAG CAGACCAGCT 1080
10 CAGGGTGTGT TCACCACTCT GGAGAAATGT AGCCACCAA GAAGGGCTCG TGTGACAGAT 1140
GCTACTGAGA CCACCATCAC CATTAGCTGG AGAACCAAGA CTGAGACGAT CACTGGCTTC 1200
CAAGTTGATG CCGTTCCAGC CAATGGCCAG ACTCCAATCC AGAGAACCAT CAAGCCAGAT 1260
GTCAGAAGCT ACACCATCAC AGGTTTACAA CCAGGCACTG ACTACAAGAT CTACCTGTAC 1320
ACCTTGAATG ACAATGCTCG GAGCTCCCCT GTGGTCATCG ACGCCTCCAC TGCCATTGAT 1380
15 GCACCATCCA ACCTGCGTTT CCTGGCCACC ACACCAATT CCTTGTGGT ATCATGGCAG 1440
CCGCCACGTG CCAGGATTAC CGGCTACATC ATCAAGTATG AGAAGCCTGG GTCTCCTCCC 1500
AGAGAAGTGG TCCCTCGGCC CCGCCTGGT GTCACAGAGG CTACTATTAC TGGCCTGGAA 1560
CCGGAACCG AATATACAAT TTATGTCATT GCCCTGAAGA ATAATCAGAA GAGCGAGCCC 1620
CTGATTGGAA GGAAAAAGAC TAGT 1644

20 SEQ. ID No. 18
LENGTH: 37
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
25 MOLECULAR TYPE: other nucleic acid (synthetic DNA)

SEQUENCE:

AAACCATGGC AGCTAGCCCC ACTGACCTGC GATTAC

37

SEQ. ID No. 19

LENGTH: 38

5 TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULAR TYPE: other nucleic acid (synthetic DNA)

SEQUENCE:

10 AAAAGATCTC TAACTAGTGG ATGGTTTGTG AATTCTG

38

SEQ. ID No. 20

LENGTH: 2481

TYPE: nucleic acid

STRANDEDNESS: double

15 TOPOLOGY: linear

MOLECULAR TYPE: other nucleic acid (DNA encoding an artificial polypeptide)

SEQUENCE:

ATGGCAGCTA GCCCCACTGA CCTGCGATTC ACCAACATTG GTCCAGACAC CATGCGTGTC 60

20 ACCTGGGCTC CACCCCATC CATTGATTTA ACCAACTTCC TGGTGCGTTA CTCACCTGTG 120

AAAAATGAGG AAGATGTTGC AGAGTTGTCA ATTTCTCCTT CAGACAATGC AGTGGTCTTA 180

ACAAATCTCC TGCCTGGTAC AGAATATGTA GTGAGTGTCT CCAGTGTCTA CGAACAACAT 240

GAGAGCACAC CTCTTAGAGG AAGACAGAAA ACAGGTCTTG ATTCCCAAC TGGCATTGAC 300

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TTTTCTGATA TTACTGCCAA CTCTTTTACT GTGCACTGGA TTGCTCCTCG AGCCACCATC 360
ACTGGCTACA GGATCCGCCA TCATCCCAG CACTTCAGTG GGAGACCTCG AGAAGATCGG 420
GTGCCCCACT CTCGGAATTC CATCACCCTC ACCAACCTCA CTCAGGCAC AGAGTATGTG 480
GTCAGCATCG TTGCTCTTAA TGGCAGAGAG GAAAGTCCCT TATTGATTGG CCAACAATCA 540
ACAGTTTCTG ATGTTCCGAG GGACCTGGAA GTTGTGTGCTG CGACCCCCAC CAGCCTACTG 600
ATCAGCTGGG ATGCTCCTGC TGTCACAGTG AGATATTACA GGATCACTTA CGGAGAAACA 660
GGAGGAAATA GCCCTGTCCA GGAGTTCACT GTGCCTGGGA GCAAGTCTAC AGCTACCATC 720
AGCGGCCTTA AACCTGGAGT TGATTATACC ATCACTGTGT ATGCTGTCAC TGGCCGTGGA 780
GACAGCCCCG CAAGCAGCAA GCCAATTTC ATTAATTACC GAACAGAAAT TGACAAACCA 840
TCCACTAGCG CTATTCTGC ACCAACTGAC CTGAAGTTCA CTCAGGTCAC ACCCACAAGC 900
CTGAGCGCCC AGTGGACACC ACCCAATGTT CAGCTCACTG GATATCGAGT GCGGGTGACC 960
CCCAAGGAGA AGACCGGACC AATGAAAGAA ATCAACCTTG CTCCTGACAG CTCATCCGTG 1020
GTTGTATCAG GACTTATGGT GGCCACCAA TATGAAGTGA GTGTCTATGC TCTTAAGGAC 1080
ACTTTGACAA GCAGACCAGC TCAGGGTGTT GTCACCACTC TGGAGAATGT CAGCCCACCA 1140
AGAAGGGCTC GTGTGACAGA TGCTACTGAG ACCACCATCA CCATTAGCTG GAGAACCAAG 1200
ACTGAGACGA TCACTGGCTT CCAAGTTGAT GCCGTTCAG CCAATGGCCA GACTCCAATC 1260
CAGAGAACCA TCAAGCCAGA TGTCAGAAAG TACACCATCA CAGGTTTACA ACCAGGCACT 1320
GACTACAAGA TCTACCTGTA CACCTTGAAT GACAATGCTC GGAGCTCCCC TGTGGTCATC 1380
GACGCCCTCA CTGCCATTGA TGCACCATCC AACCTGCGTT TCCTGGCCAC CACACCCAAT 1440
TCCTTGCTGG TATCATGGCA GCCGCCACGT GCCAGGATTA CCGGTACAT CATCAAGTAT 1500
GAGAAGCCTG GGTCTCCTCC CAGAGAAGTG GTCCCTCGGC CCCGCCCTGG TGTCACAGAG 1560
GCTACTATTA CTGGCCTGGA ACCGGGAACC GAATATACAA TTTATGTCAT TGCCCTGAAG 1620
AATAATCAGA AGAGCGAGCC CCTGATTGGA AGGAAAAAGA CTAGCGCTAT TCCTGCACCA 1680
ACTGACCTGA AGTTCACTCA GGTCACACCC ACAAGCCTGA GCGCCCAGTG GACACCACCC 1740
AATGTTGAGC TCACTGGATA TCGAGTGCGG GTGACCCCA AGGAGAAGAC CGGACCAATG 1800

AAAGAAATCA ACCTTGCTCC TGACAGCTCA TCCGTGGTTG TATCAGGACT TATGGTGGCC 1960
 ACCAAATATG AAGTGAGTGT CTATGCTCTT AAGGACACTT TGACAAGCAG ACCAGCTCAG 1920
 GGTGTTGTCA CCACTCTGGA GAATGTCAGC CCACCAAGAA GGGCTCGTGT GACAGATGCT 1980
 ACTGAGACCA CCATACCAT TAGCTGGAGA ACCAAGACTG AGACGATCAC TGGCTTCCAA 2040
 GTTGATGCCG TTCCAGCCAA TGGCCAGACT CCAATCCAGA GAACCATCAA GCCAGATGTC 2100
 AGAAGCTACA CCATCACAGG TTTACAACCA GGCCTGACT ACAAGATCTA CCTGTACACC 2160
 TTGAATGACA ATGCTCGGAG CTCCCCTGTG GTCATCGACG CCTCCACTGC CATTGATGCA 2220
 CCATCCAACC TGCCTTTCCT GGCCACCACA CCCAATTCCT TGCTGGTATC ATGGCAGCCG 2280
 CCACGTGCCA GGATTACCGG CTACATCATC AAGTATGAGA AGCCTGGGTC TCCTCCCAGA 2340
 GAAGTGGTCC CTCGGCCCCG CCCTGGTGTC ACAGAGGCTA CTATTACTGG CCTGGAACCG 2400
 GGAACCGAAT ATACAATTTA TGTCATTGCC CTGAAGAATA ATCAGAAGAG CGAGCCCCTG 2460
 ATTGGAAGGA AAAAGACTAG T 2481

SEQ. ID No. 21

LENGTH: 472

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULAR TYPE: peptide

SEQUENCE:

Pro Thr Asp Leu Arg Phe Thr Asn Ile Gly Pro Asp Thr Met Arg
 1 5 10 15
 Val Thr Trp Ala Pro Pro Pro Ser Ile Asp Leu Thr Asn Phe Leu
 20 25 30
 Val Arg Tyr Ser Pro Val Lys Asn Glu Glu Asp Val Ala Glu Leu

		35		40		45
	Ser Ile Ser Pro Ser Asp Asn Ala Val Val Leu Thr Asn Leu Leu					
		50		55		60
	Pro Gly Thr Glu Tyr Val Val Ser Val Ser Ser Val Tyr Glu Gln					
5		65		70		75
	His Glu Ser Thr Pro Leu Arg Gly Arg Gln Lys Thr Gly Leu Asp					
		80		85		90
	Ser Pro Thr Gly Ile Asp Phe Ser Asp Ile Thr Ala Asn Ser Phe					
		95		100		105
10	Thr Val His Trp Ile Ala Pro Arg Ala Thr Ile Thr Gly Tyr Arg					
		110		115		120
	Ile Arg His His Pro Glu His Phe Ser Gly Arg Pro Arg Glu Asp					
		125		130		135
	Arg Val Pro His Ser Arg Asn Ser Ile Thr Leu Thr Asn Leu Thr					
		140		145		150
15	Pro Gly Thr Glu Tyr Val Val Ser Ile Val Ala Leu Asn Gly Arg					
		155		160		165
	Glu Glu Ser Pro Leu Leu Ile Gly Gln Gln Ser Thr Val Ser Asp					
		170		175		180
20	Val Pro Arg Asp Leu Glu Val Val Ala Ala Thr Pro Thr Ser Leu					
		185		190		195
	Leu Ile Ser Trp Asp Ala Pro Ala Val Thr Val Arg Tyr Tyr Arg					
		200		205		210
	Ile Thr Tyr Gly Glu Thr Gly Gly Asn Ser Pro Val Gln Glu Phe					
25		215		220		225

	Thr Val Pro Gly Ser Lys Ser Thr Ala Thr Ile Ser Gly Leu Lys	
	230	240
	Pro Gly Val Asp Tyr Thr Ile Thr Val Tyr Ala Val Thr Gly Arg	
	245	255
5	Gly Asp Ser Pro Ala Ser Ser Lys Pro Ile Ser Ile Asn Tyr Arg	
	260	270
	Thr Glu Ile Asp Lys Pro Ser Met Ala Ile Pro Ala Pro Thr Asp	
	275	285
	Leu Lys Phe Thr Gln Val Thr Pro Thr Ser Leu Ser Ala Gln Trp	
10	290	300
	Thr Pro Pro Asn Val Gln Leu Thr Gly Tyr Arg Val Arg Val Thr	
	305	315
	Pro Lys Glu Lys Thr Gly Pro Met Lys Glu Ile Asn Leu Ala Pro	
	320	330
15	Asp Ser Ser Ser Val Val Val Ser Gly Leu Met Val Ala Thr Lys	
	335	345
	Tyr Glu Val Ser Val Tyr Ala Leu Lys Asp Thr Leu Thr Ser Arg	
	350	360
	Pro Ala Gln Gly Val Val Thr Thr Leu Glu Asn Val Ser Pro Pro	
20	365	375
	Arg Arg Ala Arg Val Thr Asp Ala Thr Glu Thr Thr Ile Thr Ile	
	380	390
	Ser Trp Arg Thr Lys Thr Glu Thr Ile Thr Gly Phe Gln Val Asp	
	395	405
25	Ala Val Pro Ala Asn Gly Gln Thr Pro Ile Gln Arg Thr Ile Lys	

	410	415	420
Pro Asp Val Arg Ser Tyr Thr Ile Thr Gly Leu Gln Pro Gly Thr			
	425	430	435
Asp Tyr Lys Ile Tyr Leu Tyr Thr Leu Asn Asp Asn Ala Arg Ser			
5	440	445	450
Ser Pro Val Val Ile Asp Ala Ser Thr Ala Ile Asp Ala Pro Ser			
	455	460	465
Asn Leu Arg Phe Leu Ala Thr			
	470		

10 SEQ. ID No. 22

LENGTH: 457

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

15 MOLECULAR TYPE: peptide

SEQUENCE:

Pro Thr Asp Leu Arg Phe Thr Asn Ile Gly Pro Asp Thr Met Arg			
1	5	10	15
Val Thr Trp Ala Pro Pro Pro Ser Ile Asp Leu Thr Asn Phe Leu			
20	20	25	30
Val Arg Tyr Ser Pro Val Lys Asn Glu Glu Asp Val Ala Glu Leu			
	35	40	45
Ser Ile Ser Pro Ser Asp Asn Ala Val Val Leu Thr Asn Leu Leu			
	50	55	60

	Pro	Gly	Thr	Glu	Tyr	Val	Val	Ser	Val	Ser	Ser	Val	Tyr	Glu	Gln
						65				70					75
	His	Glu	Ser	Thr	Pro	Leu	Arg	Gly	Arg	Gln	Lys	Thr	Gly	Leu	Asp
						80				85					90
5	Ser	Pro	Thr	Gly	Ile	Asp	Phe	Ser	Asp	Ile	Thr	Ala	Asn	Ser	Phe
						95				100					105
	Thr	Val	His	Trp	Ile	Ala	Pro	Arg	Ala	Thr	Ile	Thr	Gly	Tyr	Arg
						110				115					120
	Ile	Arg	His	His	Pro	Glu	His	Phe	Ser	Gly	Arg	Pro	Arg	Glu	Asp
10						125				130					135
	Arg	Val	Pro	His	Ser	Arg	Asn	Ser	Ile	Thr	Leu	Thr	Asn	Leu	Thr
						140				145					150
	Pro	Gly	Thr	Glu	Tyr	Val	Val	Ser	Ile	Val	Ala	Leu	Asn	Gly	Arg
						155				160					165
	Glu	Glu	Ser	Pro	Leu	Leu	Ile	Gly	Gln	Gln	Ser	Thr	Val	Ser	Asp
						170				175					180
	Val	Pro	Arg	Asp	Leu	Glu	Val	Val	Ala	Ala	Thr	Pro	Thr	Ser	Leu
						185				190					195
	Leu	Ile	Ser	Trp	Asp	Ala	Pro	Ala	Val	Thr	Val	Arg	Tyr	Tyr	Arg
20						200				205					210
	Ile	Thr	Tyr	Gly	Glu	Thr	Gly	Gly	Asn	Ser	Pro	Val	Gln	Glu	Phe
						215				220					225
	Thr	Val	Pro	Gly	Ser	Lys	Ser	Thr	Ala	Thr	Ile	Ser	Gly	Leu	Lys
						230				235					240
25	Pro	Gly	Val	Asp	Tyr	Thr	Ile	Thr	Val	Tyr	Ala	Val	Thr	Gly	Arg

	245	250	255
	Gly Asp Ser Pro Ala Ser Ser Lys Pro Ile Ser Ile Asn Tyr Arg		
	260	265	270
	Thr Glu Ile Asp Lys Pro Ser Met Asn Val Ser Pro Pro Arg Arg		
5	275	280	285
	Ala Arg Val Thr Asp Ala Thr Glu Thr Thr Ile Thr Ile Ser Trp		
	290	295	300
	Arg Thr Lys Thr Glu Thr Ile Thr Gly Phe Gln Val Asp Ala Val		
	305	310	315
10	Pro Ala Asn Gly Gln Thr Pro Ile Gln Arg Thr Ile Lys Pro Asp		
	320	325	330
	Val Arg Ser Tyr Thr Ile Thr Gly Leu Gln Pro Gly Thr Asp Tyr		
	335	340	345
	Lys Ile Tyr Leu Tyr Thr Leu Asn Asp Asn Ala Arg Ser Ser Pro		
15	350	355	360
	Val Val Ile Asp Ala Ser Thr Ala Ile Asp Ala Pro Ser Asn Leu		
	365	370	375
	Arg Phe Leu Ala Thr Thr Pro Asn Ser Leu Leu Val Ser Trp Gln		
	380	385	390
20	Pro Pro Arg Ala Arg Ile Thr Gly Tyr Ile Ile Lys Tyr Glu Lys		
	395	400	405
	Pro Gly Ser Pro Pro Arg Glu Val Val Pro Arg Pro Arg Pro Gly		
	410	415	420
	Val Thr Glu Ala Thr Ile Thr Gly Leu Glu Pro Gly Thr Glu Tyr		
25	425	430	435

Thr Ile Tyr Val Ile Ala Leu Lys Asn Asn Gln Lys Ser Glu Pro
 440 445 450
 Leu Ile Gly Arg Lys Lys Thr
 455

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SEQ. ID No. 23

LENGTH: 549

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULAR TYPE: peptide

SEQUENCE:

Pro	Thr	Asp	Leu	Arg	Phe	Thr	Asn	Ile	Gly	Pro	Asp	Thr	Met	Arg
1					5				10					15
Val	Thr	Trp	Ala	Pro	Pro	Pro	Ser	Ile	Asp	Leu	Thr	Asn	Phe	Leu
					20				25					30
Val	Arg	Tyr	Ser	Pro	Val	Lys	Asn	Glu	Glu	Asp	Val	Ala	Glu	Leu
					35				40					45
Ser	Ile	Ser	Pro	Ser	Asp	Asn	Ala	Val	Val	Leu	Thr	Asn	Leu	Leu
					50				55					60
Pro	Gly	Thr	Glu	Tyr	Val	Val	Ser	Val	Ser	Ser	Val	Tyr	Glu	Gln
					65				70					75
His	Glu	Ser	Thr	Pro	Leu	Arg	Gly	Arg	Gln	Lys	Thr	Gly	Leu	Asp
					80				85					90
Ser	Pro	Thr	Gly	Ile	Asp	Phe	Ser	Asp	Ile	Thr	Ala	Asn	Ser	Phe

15

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	95	100	105
	Thr Val His Trp Ile Ala Pro Arg Ala Thr Ile Thr Gly Tyr Arg		
	110	115	120
	Ile Arg His His Pro Glu His Phe Ser Gly Arg Pro Arg Glu Asp		
5	125	130	135
	Arg Val Pro His Ser Arg Asn Ser Ile Thr Leu Thr Asn Leu Thr		
	140	145	150
	Pro Gly Thr Glu Tyr Val Val Ser Ile Val Ala Leu Asn Gly Arg		
	155	160	165
10	Glu Glu Ser Pro Leu Leu Ile Gly Gln Gln Ser Thr Val Ser Asp		
	170	175	180
	Val Pro Arg Asp Leu Glu Val Val Ala Ala Thr Pro Thr Ser Leu		
	185	190	195
	Leu Ile Ser Trp Asp Ala Pro Ala Val Thr Val Arg Tyr Tyr Arg		
15	200	205	210
	Ile Thr Tyr Gly Glu Thr Gly Gly Asn Ser Pro Val Gln Glu Phe		
	215	220	225
	Thr Val Pro Gly Ser Lys Ser Thr Ala Thr Ile Ser Gly Leu Lys		
	230	235	240
20	Pro Gly Val Asp Tyr Thr Ile Thr Val Tyr Ala Val Thr Gly Arg		
	245	250	255
	Gly Asp Ser Pro Ala Ser Ser Lys Pro Ile Ser Ile Asn Tyr Arg		
	260	265	270
	Thr Glu Ile Asp Lys Pro Ser Met Ala Ile Pro Ala Pro Thr Asp		
25	275	280	285

	Leu	Lys	Phe	Thr	Gln	Val	Thr	Pro	Thr	Ser	Leu	Ser	Ala	Gln	Trp
					290					295					300
	Thr	Pro	Pro	Asn	Val	Gln	Leu	Thr	Gly	Tyr	Arg	Val	Arg	Val	Thr
					305					310					315
5	Pro	Lys	Glu	Lys	Thr	Gly	Pro	Met	Lys	Glu	Ile	Asn	Leu	Ala	Pro
					320					325					330
	Asp	Ser	Ser	Ser	Val	Val	Val	Ser	Gly	Leu	Met	Val	Ala	Thr	Lys
					335					340					345
	Tyr	Glu	Val	Ser	Val	Tyr	Ala	Leu	Lys	Asp	Thr	Leu	Thr	Ser	Arg
10					350					355					360
	Pro	Ala	Gln	Gly	Val	Val	Thr	Thr	Leu	Glu	Asn	Val	Ser	Pro	Pro
					365					370					375
	Arg	Arg	Ala	Arg	Val	Thr	Asp	Ala	Thr	Glu	Thr	Thr	Ile	Thr	Ile
					380					385					390
15	Ser	Trp	Arg	Thr	Lys	Thr	Glu	Thr	Ile	Thr	Gly	Phe	Gln	Val	Asp
					395					400					405
	Ala	Val	Pro	Ala	Asn	Gly	Gln	Thr	Pro	Ile	Gln	Arg	Thr	Ile	Lys
					410					415					420
	Pro	Asp	Val	Arg	Ser	Tyr	Thr	Ile	Thr	Gly	Leu	Gln	Pro	Gly	Thr
20					425					430					435
	Asp	Tyr	Lys	Ile	Tyr	Leu	Tyr	Thr	Leu	Asn	Asp	Asn	Ala	Arg	Ser
					440					445					450
	Ser	Pro	Val	Val	Ile	Asp	Ala	Ser	Thr	Ala	Ile	Asp	Ala	Pro	Ser
					455					460					465
25	Asn	Leu	Arg	Phe	Leu	Ala	Thr	Thr	Pro	Asn	Ser	Leu	Leu	Val	Ser

	470	475	480
	Trp Gln Pro Pro Arg Ala Arg Ile Thr Gly Tyr Ile Ile Lys Tyr		
	485	490	495
	Glu Lys Pro Gly Ser Pro Pro Arg Glu Val Val Pro Arg Pro Arg		
5	500	505	510
	Pro Gly Val Thr Glu Ala Thr Ile Thr Gly Leu Glu Pro Gly Thr		
	515	520	525
	Glu Tyr Thr Ile Tyr Val Ile Ala Leu Lys Asn Asn Gln Lys Ser		
	530	535	540
10	Glu Pro Leu Ile Gly Arg Lys Lys Thr		
	545		

SEQ. ID No. 24

LENGTH: 574

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULAR TYPE: peptide

SEQUENCE:

	Pro Thr Asp Leu Arg Phe Thr Asn Ile Gly Pro Asp Thr Met Arg
20	1 5 10 15
	Val Thr Trp Ala Pro Pro Pro Ser Ile Asp Leu Thr Asn Phe Leu
	20 25 30
	Val Arg Tyr Ser Pro Val Lys Asn Glu Glu Asp Val Ala Glu Leu
	35 40 45

	Ser	Ile	Ser	Pro	Ser	Asp	Asn	Ala	Val	Val	Leu	Thr	Asn	Leu	Leu
					50					55					60
	Pro	Gly	Thr	Glu	Tyr	Val	Val	Ser	Val	Ser	Ser	Val	Tyr	Glu	Gln
					65					70					75
5	His	Glu	Ser	Thr	Pro	Leu	Arg	Gly	Arg	Gln	Lys	Thr	Gly	Leu	Asp
					80					85					90
	Ser	Pro	Thr	Gly	Ile	Asp	Phe	Ser	Asp	Ile	Thr	Ala	Asn	Ser	Phe
					95					100					105
	Thr	Val	His	Trp	Ile	Ala	Pro	Arg	Ala	Thr	Ile	Thr	Gly	Tyr	Arg
10					110					115					120
	Ile	Arg	His	His	Pro	Glu	His	Phe	Ser	Gly	Arg	Pro	Arg	Glu	Asp
					125					130					135
	Arg	Val	Pro	His	Ser	Arg	Asn	Ser	Ile	Thr	Leu	Thr	Asn	Leu	Thr
					140					145					150
15	Pro	Gly	Thr	Glu	Tyr	Val	Val	Ser	Ile	Val	Ala	Leu	Asn	Gly	Arg
					155					160					165
	Glu	Glu	Ser	Pro	Leu	Leu	Ile	Gly	Gln	Gln	Ser	Thr	Val	Ser	Asp
					170					175					180
	Val	Pro	Arg	Asp	Leu	Glu	Val	Val	Ala	Ala	Thr	Pro	Thr	Ser	Leu
20					185					190					195
	Leu	Ile	Ser	Trp	Asp	Ala	Pro	Ala	Val	Thr	Val	Arg	Tyr	Tyr	Arg
					200					205					210
	Ile	Thr	Tyr	Gly	Glu	Thr	Gly	Gly	Asn	Ser	Pro	Val	Gln	Glu	Phe
					215					220					225
25	Thr	Val	Pro	Gly	Ser	Lys	Ser	Thr	Ala	Thr	Ile	Ser	Gly	Leu	Lys

		230		235		240
	Pro Gly Val Asp Tyr Thr Ile Thr Val Tyr Ala Val Thr Gly Arg					
		245		250		255
	Gly Asp Ser Pro Ala Ser Ser Lys Pro Ile Ser Ile Asn Tyr Arg					
5		260		265		270
	Thr Glu Ile Asp Lys Pro Ser Met Ala Ile Pro Ala Pro Thr Asp					
		275		280		285
	Leu Lys Phe Thr Gln Val Thr Pro Thr Ser Leu Ser Ala Gln Trp					
		290		295		300
10	Thr Pro Pro Asn Val Gln Leu Thr Gly Tyr Arg Val Arg Val Thr					
		305		310		315
	Pro Lys Glu Lys Thr Gly Pro Met Lys Glu Ile Asn Leu Ala Pro					
		320		325		330
	Asp Ser Ser Ser Val Val Val Ser Gly Leu Met Val Ala Thr Lys					
15		335		340		345
	Tyr Glu Val Ser Val Tyr Ala Leu Lys Asp Thr Leu Thr Ser Arg					
		350		355		360
	Pro Ala Gln Gly Val Val Thr Thr Leu Glu Asn Val Ser Pro Pro					
		365		370		375
20	Arg Arg Ala Arg Val Thr Asp Ala Thr Glu Thr Thr Ile Thr Ile					
		380		385		390
	Ser Trp Arg Thr Lys Thr Glu Thr Ile Thr Gly Phe Gln Val Asp					
		395		400		405
	Ala Val Pro Ala Asn Gly Gln Thr Pro Ile Gln Arg Thr Ile Lys					
25		410		415		420

	Pro Asp Val Arg Ser Tyr Thr Ile Thr Gly Leu Gln Pro Gly Thr		
	425	430	435
	Asp Tyr Lys Ile Tyr Leu Tyr Thr Leu Asn Asp Asn Ala Arg Ser		
	440	445	450
5	Ser Pro Val Val Ile Asp Ala Ser Thr Ala Ile Asp Ala Pro Ser		
	455	460	465
	Asn Leu Arg Phe Leu Ala Thr Thr Pro Asn Ser Leu Leu Val Ser		
	470	475	480
	Trp Gln Pro Pro Arg Ala Arg Ile Thr Gly Tyr Ile Ile Lys Tyr		
10	485	490	495
	Glu Lys Pro Gly Ser Pro Pro Arg Glu Val Val Pro Arg Pro Arg		
	500	505	510
	Pro Gly Val Thr Glu Ala Thr Ile Thr Gly Leu Glu Pro Gly Thr		
	515	520	525
15	Glu Tyr Thr Ile Tyr Val Ile Ala Leu Lys Asn Asn Gln Lys Ser		
	530	535	540
	Glu Pro Leu Ile Gly Arg Lys Lys Thr Asp Glu Leu Pro Gln Leu		
	545	550	555
	Val Thr Leu Pro His Pro Asn Leu His Gly Pro Glu Ile Leu Asp		
20	560	565	570
	Val Pro Ser Thr		

SEQ. ID No. 25

LENGTH: 274

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULAR TYPE: peptide

SEQUENCE:

5	Pro Thr Asp Leu Arg Phe Thr Asn Ile Gly Pro Asp Thr Met Arg	
	1 5 10 15	
	Val Thr Trp Ala Pro Pro Pro Ser Ile Asp Leu Thr Asn Phe Leu	
	20 25 30	
	Val Arg Tyr Ser Pro Val Lys Asn Glu Glu Asp Val Ala Glu Leu	
10	35 40 45	
	Ser Ile Ser Pro Ser Asp Asn Ala Val Val Leu Thr Asn Leu Leu	
	50 55 60	
	Pro Gly Thr Glu Tyr Val Val Ser Val Ser Ser Val Tyr Glu Gln	
	65 70 75	
15	His Glu Ser Thr Pro Leu Arg Gly Arg Gln Lys Thr Gly Leu Asp	
	80 85 90	
	Ser Pro Thr Gly Ile Asp Phe Ser Asp Ile Thr Ala Asn Ser Phe	
	95 100 105	
	Thr Val His Trp Ile Ala Pro Arg Ala Thr Ile Thr Gly Tyr Arg	
20	110 115 120	
	Ile Arg His His Pro Glu His Phe Ser Gly Arg Pro Arg Glu Asp	
	125 130 135	
	Arg Val Pro His Ser Arg Asn Ser Ile Thr Leu Thr Asn Leu Thr	
	140 145 150	
25	Pro Gly Thr Glu Tyr Val Val Ser Ile Val Ala Leu Asn Gly Arg	

	155	160	165
	Glu Glu Ser Pro Leu Leu Ile Gly Gln Gln Ser Thr Val Ser Asp		
	170	175	180
	Val Pro Arg Asp Leu Glu Val Val Ala Ala Thr Pro Thr Ser Leu		
5	185	190	195
	Leu Ile Ser Trp Asp Ala Pro Ala Val Thr Val Arg Tyr Tyr Arg		
	200	205	210
	Ile Thr Tyr Gly Glu Thr Gly Gly Asn Ser Pro Val Gln Glu Phe		
	215	220	225
10	Thr Val Pro Gly Ser Lys Ser Thr Ala Thr Ile Ser Gly Leu Lys		
	230	235	240
	Pro Gly Val Asp Tyr Thr Ile Thr Val Tyr Ala Val Thr Gly Arg		
	245	250	255
	Gly Asp Ser Pro Ala Ser Ser Lys Pro Ile Ser Ile Asn Tyr Arg		
15	260	265	270
	Thr Glu Ile Asp		

SEQ. ID No. 26

LENGTH: 1374

TYPE: nucleic acid

20 STRANDEDNESS: double

TOPOLOGY: linear

MOLECULAR TYPE: other nucleic acid (DNA encoding an artificial polypeptide)

SEQUENCE:

ATGCCCACTG ACCTGCGATT CACCAACATT GGTCCAGACA CCATGCGTGT CACCTGGGCT 60
CCACCCCCAT CCATTGATTT AACCAACTTC CTGGTGC GTT ACTCACCTGT GAAAAATGAG 120
GAAGATGTTG CAGAGTTGTC AATTTCTCCT TCAGACAATG CAGTGGTCTT AACAAATCTC 180
CTGCCTGGTA CAGAATATGT AGTGAGTGTC TCCAGTGTCT ACGAACAACA TGAGAGCACA 240
5 CCTCTTAGAG GAAGACAGAA AACAGTCTT GATTCCCCAA CTGGCATTGA CTTTTCTGAT 300
ATTACTGCCA ACTCTTTTAC TGTGCACTGG ATTGCTCCTC GAGCCACCAT CACTGGCTAC 360
AGGATCCGCC ATCATCCCGA GCACCTCAGT GGGAGACCTC GAGAAGATCG GGTGCCCCAC 420
TCTCGGAATT CCATCACCTT CACCAACCTC ACTCCAGGCA CAGAGTATGT GGTGAGCATC 480
GTTGCTCTTA ATGGCAGAGA GGAAGTCCC TTATTGATTG GCCAACAAATC AACAGTTTCT 540
10 GATGTTCGA GGGACCTGGA AGTTGTTGCT GCGACCCCCA CCAGCCTACT GATCAGCTGG 600
GATGCTCCTG CTGTACAGT GAGATATTAC AGGATCACTT ACGGAGAAAC AGGAGGAAAT 660
AGCCCTGTCC AGGAGTTCAC TGTGCCTGGG AGCAAGTCTA CAGCTACCAT CAGCGGCCCT 720
AAACCTGGAG TTGATTATAC CATCACTGTG TATGCTGTCA CTGGCCGTGG AGACAGCCCC 780
GCAAGCAGCA AGCCAATTTC CATTAATTAC CGAACAGAAA TTGACAAACC ATCCATGGCA 840
15 GCCGGGAGCA TCAACACGCT GCCCGCCTTG CCCGAGGATG GCGGCAGCGG GCGCTTCCCG 900
CCCGGCCACT TCAAGGACCC CAAGCGGCTG TACTGCAAAA ACGGGGGCTT CTTCCTGCGC 960
ATCCACCCCG ACGGCCGAGT TGACGGGGTC CGGGAGAAGA GCGACCCTCA CATCAAGCTA 1020
CAACTTCAAG CAGAAGAGAG AGGAGTTGTG TCTATCAAAG GAGTGTGTGC TAACCGTTAC 1080
CTGGCTATGA AGGAAGATGG AAGATTACTG GCTTCTAAAT GTGTTACGGA TGAGTGTTC 1140
20 TTTTTTGAAC GATTGGAATC TAATAACTAC AATACTTACC GCTCAAGGAA ATACACCACT 1200
TGGTATGTGG CACTGAAACG AACTGGGCAG TATAAACTTG GATCCAAAAC AGGACCTGGG 1260
CAGAAAGCTA TACTTTTTCT TCCAATGTCT GCTGCTAGCG ACGAGCTTCC CCAACTGGTA 1320
ACCTTCCAC ACCCAATCT TCATGGACCA GAGATCTTGG ATGTTCTCTC CACA 1374

LENGTH: 1416

TYPE: nucleic acid

STRANDEDNESS: double

TOPOLOGY: linear

5 MOLECULAR TYPE: other nucleic acid (DNA encoding an artificial polypeptide)

SEQUENCE:

10 CCCACTGACC TGCGATTAC CAACATTGGT CCAGACACCA TGCGTGTCAC CTGGGCTCCA 60
CCCCCATCCA TTGATTTAAC CAACTTCCTG GTGCGTTACT CACCTGTGAA AAATGAGGAA 120
15 GATGTTGACAG AGTTGTCAAT TTCTCCTTCA GACAATGCAG TGGTCTTAAC AAATCTCCTG 180
CCTGGTACAG AATATGTAGT GAGTGTCTCC AGTGTCTACG AACAAACATGA GAGCACACCT 240
CTTAGAGGAA GACAGAAAAC AGGTCTTGAT TCCCCAACTG GCATTGACTT TTCTGATATT 300
ACTGCCAACT CTTTACTGT GCACTGGATT GCTCCTCGAG CCACCATCAC TGGCTACAGG 360
ATCCGCCATC ATCCCGAGCA CTTCACTGGG AGACCTCGAG AAGATCGGGT GCCCACTCT 420
15 CGGAATTCCA TCACCCTCAC CAACCTCACT CCAGGCACAG AGTATGTGGT CAGCATCGTT 480
GCTCTTAATG GCAGAGAGGA AAGTCCCTTA TTGATTGGCC AACAAATCAAC AGTTTCTGAT 540
GTTCCGAGGG ACCTGGAAGT TGTGCTGCG ACCCCACCA GCTACTGAT CAGCTGGGAT 600
GCTCCTGCTG TCACAGTGAG ATATTACAGG ATCACTTACG GAGAAACAGG AGGAAATAGC 660
CCTGTCCAGG AGTTCCTGT GCCTGGGAGC AAGTCTACAG CTACCATCAG CGGCCTTAAA 720
20 CCTGGAGTTG ATTATACCAT CACTGTGTAT GCTGTCACTG GCCGTGGAGA CAGCCCCGCA 780
AGCAGCAAGC CAATTTCCAT TAATTACCGA ACAGAAATTG ACAAAACATC CATGGCTATT 840
CCTGCACCAA CTGACCTGAA GTTCACTCAG GTCACACCCA CAAGCCTGAG CGCCCACTGG 900
ACACCACCCA ATGTTAGCT CACTGGATAT CGAGTGCGGG TGACCCCCAA GGAGAAGACC 960
GGACCAATGA AAGAAATCAA CCTTGCTCCT GACAGCTCAT CCGTGTTGT ATCAGGACTT 020
25 ATGGTGGCCA CCAAATATGA AGTGAGTGTC TATGCTCTTA AGGACACTTT GACAAGCAGA 1080

CCAGCTCAGG GTGTTGTCAC CACTCTGGAG AATGTCAGCC CACCAAGAAG GGCTCGTGTG 1140
ACAGATGCTA CTGAGACCAC CATCACCATT AGCTGGAGAA CCAAGACTGA GACGATCACT 1200
GGCTTCCAAG TTGATGCCGT TCCAGCCAAT GGCCAGACTC CAATCCAGAG AACCATCAAG 1260
CCAGATGTCA GAAGCTACAC CATCACAGGT TTACAACCAG GCACTGACTA CAAGATCTAC 1320
5 CTGTACACCT TGAATGACAA TGCTCGGAGC TCCCTGTGG TCATCGACGC CTCCACTGCC 1380
ATTGATGCAC CATCCAACCT GCGTTTCCTG GCCACC 1416

SEQ. ID No. 28

LENGTH: 35

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULAR TYPE: peptide

SEQUENCE:

Gly Gly Arg Gly Thr Pro Gly Lys Pro Gly Pro Arg Gly Gln Arg

Gly Pro Thr Gly Pro Arg Gly Glu Arg Gly Pro Arg Gly Ile Thr

Gly Lys Pro Gly Pro

SEQ. ID No. 29

LENGTH: 302

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULAR TYPE: peptide

SEQUENCE:

	Pro	Thr	Asp	Leu	Arg	Phe	Thr	Asn	Ile	Gly	Pro	Asp	Thr	Met	Arg
5	1				5					10					15
	Val	Thr	Trp	Ala	Pro	Pro	Pro	Ser	Ile	Asp	Leu	Thr	Asn	Phe	Leu
					20					25					30
	Val	Arg	Tyr	Ser	Pro	Val	Lys	Asn	Glu	Glu	Asp	Val	Ala	Glu	Leu
					35					40					45
10	Ser	Ile	Ser	Pro	Ser	Asp	Asn	Ala	Val	Val	Leu	Thr	Asn	Leu	Leu
					50					55					60
	Pro	Gly	Thr	Glu	Tyr	Val	Val	Ser	Val	Ser	Ser	Val	Tyr	Glu	Gln
					65					70					75
	His	Glu	Ser	Thr	Pro	Leu	Arg	Gly	Arg	Gln	Lys	Thr	Gly	Leu	Asp
15					80					85					90
	Ser	Pro	Thr	Gly	Ile	Asp	Phe	Ser	Asp	Ile	Thr	Ala	Asn	Ser	Phe
					95					100					105
	Thr	Val	His	Trp	Ile	Ala	Pro	Arg	Ala	Thr	Ile	Thr	Gly	Tyr	Arg
					110					115					120
20	Ile	Arg	His	His	Pro	Glu	His	Phe	Ser	Gly	Arg	Pro	Arg	Glu	Asp
					125					130					135
	Arg	Val	Pro	His	Ser	Arg	Asn	Ser	Ile	Thr	Leu	Thr	Asn	Leu	Thr
					140					145					150
	Pro	Gly	Thr	Glu	Tyr	Val	Val	Ser	Ile	Val	Ala	Leu	Asn	Gly	Arg
25					155					160					165

Glu Glu Ser Pro Leu Leu Ile Gly Gln Gln Ser Thr Val Ser Asp		
	170	175
Val Pro Arg Asp Leu Glu Val Val Ala Ala Thr Pro Thr Ser Leu		
	185	190
5 Leu Ile Ser Trp Asp Ala Pro Ala Val Thr Val Arg Tyr Tyr Arg		
	200	205
Ile Thr Tyr Gly Glu Thr Gly Gly Asn Ser Pro Val Gln Glu Phe		
	215	220
Thr Val Pro Gly Ser Lys Ser Thr Ala Thr Ile Ser Gly Leu Lys		
	230	235
Pro Gly Val Asp Tyr Thr Ile Thr Val Tyr Ala Val Thr Gly Arg		
	245	250
Gly Asp Ser Pro Ala Ser Ser Lys Pro Ile Ser Ile Asn Tyr Arg		
	260	265
15 Thr Glu Ile Asp Lys Pro Ser Asp Glu Leu Pro Gln Leu Val Thr		
	275	280
Leu Pro His Pro Asn Leu His Gly Pro Glu Ile Leu Asp Val Pro		
	290	295
Ser Thr		300

20 SEQ. ID No. 30

LENGTH: 573

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULAR TYPE: peptide

SEQUENCE:

	Met	Ala	Ala	Ser	Ala	Ile	Pro	Ala	Pro	Thr	Asp	Leu	Lys	Phe	Thr	
					5					10					15	
5	Gln	Val	Thr	Pro	Thr	Ser	Leu	Ser	Ala	Gln	Trp	Thr	Pro	Pro	Asn	
					20					25					30	
	Val	Gln	Leu	Thr	Gly	Tyr	Arg	Val	Arg	Val	Thr	Pro	Lys	Glu	Lys	
					35					40					45	
	Thr	Gly	Pro	Met	Lys	Glu	Ile	Asn	Leu	Ala	Pro	Asp	Ser	Ser	Ser	
10					50					55					60	
	Val	Val	Val	Ser	Gly	Leu	Met	Val	Ala	Thr	Lys	Tyr	Glu	Val	Ser	
					65					70					75	
	Val	Tyr	Ala	Leu	Lys	Asp	Thr	Leu	Thr	Ser	Arg	Pro	Ala	Gln	Gly	
					80					85					90	
15	Val	Val	Thr	Thr	Leu	Glu	Asn	Val	Ser	Pro	Pro	Arg	Arg	Ala	Arg	
					95					100					105	
	Val	Thr	Asp	Ala	Thr	Glu	Thr	Thr	Ile	Thr	Ile	Ser	Trp	Arg	Thr	
					110					115					120	
	Lys	Thr	Glu	Thr	Ile	Thr	Gly	Phe	Gln	Val	Asp	Ala	Val	Pro	Ala	
20					125					130					135	
	Asn	Gly	Gln	Thr	Pro	Ile	Gln	Arg	Thr	Ile	Lys	Pro	Asp	Val	Arg	
					140					145					150	
	Ser	Tyr	Thr	Ile	Thr	Gly	Leu	Gln	Pro	Gly	Thr	Asp	Tyr	Lys	Ile	
					155					160					165	
25	Tyr	Leu	Tyr	Thr	Leu	Asn	Asp	Asn	Ala	Arg	Ser	Ser	Pro	Val	Val	

	170	175	180
Ile Asp Ala Ser Thr Ala Ile Asp Ala Pro Ser Asn Leu Arg Phe			
	185	190	195
Leu Ala Thr Thr Pro Asn Ser Leu Leu Val Ser Trp Gln Pro Pro			
5	200	205	210
Arg Ala Arg Ile Thr Gly Tyr Ile Ile Lys Tyr Glu Lys Pro Gly			
	215	220	225
Ser Pro Pro Arg Glu Val Val Pro Arg Pro Arg Pro Gly Val Thr			
	230	235	240
10 Glu Ala Thr Ile Thr Gly Leu Glu Pro Gly Thr Glu Tyr Thr Ile			
	245	250	255
Tyr Val Ile Ala Leu Lys Asn Asn Gln Lys Ser Glu Pro Leu Ile			
	260	265	270
Gly Arg Lys Lys Thr Ala Ile Pro Ala Pro Thr Asp Leu Lys Phe			
	275	280	285
15 Thr Gln Val Thr Pro Thr Ser Leu Ser Ala Gln Trp Thr Pro Pro			
	290	295	300
Asn Val Gln Leu Thr Gly Tyr Arg Val Arg Val Thr Pro Lys Glu			
	305	310	315
20 Lys Thr Gly Pro Met Lys Glu Ile Asn Leu Ala Pro Asp Ser Ser			
	320	325	330
Ser Val Val Val Ser Gly Leu Met Val Ala Thr Lys Tyr Glu Val			
	335	340	345
Ser Val Tyr Ala Leu Lys Asp Thr Leu Thr Ser Arg Pro Ala Gln			
25	350	355	360

	Gly Val Val Thr Thr Leu Glu Asn Val Ser Pro Pro Arg Arg Ala		
		365	370 375
	Arg Val Thr Asp Ala Thr Glu Thr Thr Ile Thr Ile Ser Trp Arg		
		380	385 390
5	Thr Lys Thr Glu Thr Ile Thr Gly Phe Gln Val Asp Ala Val Pro		
		395	400 405
	Ala Asn Gly Gln Thr Pro Ile Gln Arg Thr Ile Lys Pro Asp Val		
		410	415 420
	Arg Ser Tyr Thr Ile Thr Gly Leu Gln Pro Gly Thr Asp Tyr Lys		
10		425	430 435
	Ile Tyr Leu Tyr Thr Leu Asn Asp Asn Ala Arg Ser Ser Pro Val		
		440	445 450
	Val Ile Asp Ala Ser Thr Ala Ile Asp Ala Pro Ser Asn Leu Arg		
		455	460 465
15	Phe Leu Ala Thr Thr Pro Asn Ser Leu Leu Val Ser Trp Gln Pro		
		470	475 480
	Pro Arg Ala Arg Ile Thr Gly Tyr Ile Ile Lys Tyr Glu Lys Pro		
		485	490 495
	Gly Ser Pro Pro Arg Glu Val Val Pro Arg Pro Arg Pro Gly Val		
20		500	505 510
	Thr Glu Ala Thr Ile Thr Gly Leu Glu Pro Gly Thr Glu Tyr Thr		
		515	520 525
	Ile Tyr Val Ile Ala Leu Lys Asn Asn Gln Lys Ser Glu Pro Leu		
		530	535 540
25	Ile Gly Arg Lys Lys Thr Ser Asp Glu Leu Pro Gln Leu Val Thr		

	545	550	555
Leu Pro His Pro Asn Leu His Gly Pro Glu Ile Leu Asp Val Pro			
	560	565	570
Ser Thr Ser			

5 SEQ. ID No. 31

LENGTH: 37

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

10 MOLECULAR TYPE: other nucleic acid (synthetic DNA)

SEQUENCE:

AAACCATGGC AGCTAGCAAT GTCAGCCCAC CAAGAAG 37

SEQ. ID No. 32

LENGTH: 37

15 TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULAR TYPE: other nucleic acid (synthetic DNA)

SEQUENCE:

20 AAAGGATCCC TAACTAGTGG AAGGAACATC CAAGATC 37

SEQ. ID No. 33

LENGTH: 1722

TYPE: nucleic acid

STRANDEDNESS: double

TOPOLOGY: linear

MOLECULAR TYPE: other nucleic acid (DNA encoding an artificial polypeptide)

SEQUENCE:

ATGGCAGCTA GCGCTATTCC TGCACCAACT GACCTGAAGT TCACTCAGGT CACACCCACA 60
AGCCTGAGCG CCCAGTGGAC ACCACCCAAT GTTCAGCTCA CTGGATATCG AGTGCGGGTG 120
ACCCCCAAGG AGAAGACCGG ACCAATGAAA GAAATCAACC TTGCTCCTGA CAGCTCATCC 180
GTGGTTGTAT CAGGACTTAT GGTGGCCACC AAATATGAAG TGAGTGTCTA TGCTCTTAAG 240
GACACTTTGA CAAGCAGACC AGCTCAGGGT GTTGTCACCA CTCTGGAGAA TGTGAGCCCA 300
CCAAGAAGGG CTCGTGTGAC AGATGCTACT GAGACCACCA TCACCATTAG CTGGAGAACC 360
AAGACTGAGA CGATCACTGG CTTCCAAGTT GATGCCGTTC CAGCCAATGG CCAGACTCCA 420
ATCCAGAGAA CCATCAAGCC AGATGTCAGA AGCTACACCA TCACAGGTTT ACAACCAGGC 480
ACTGACTACA AGATCTACCT GTACACCTTG AATGACAATG CTCGGAGCTC CCCTGTGGTC 540
ATCGACGCCT CCACTGCCAT TGATGCACCA TCCAACCTGC GTTTCCTGGC CACCACACCC 600
AATTCCTTGC TGGTATCATG GCAGCCGCCA CGTGCCAGGA TTACCGGCTA CATCATCAAG 660
TATGAGAAGC CTGGGTCTCC TCCCAGAGAA GTGGTCCCTC GGCCCCGCCC TGGTGTACCA 720
GAGGCTACTA TTACTGGCCT GGAACCGGGA ACCGAATATA CAATTTATGT CATTGCCCTG 780
AAGAATAATC AGAAGAGCGA GCCCCTGATT GGAAGGAAAA AGACTAGCGC TATTCTGCA 840
CCAAGTGACC TGAAGTTCAC TCAGGTCACA CCCACAAGCC TGAGCGCCCA GTGGACACCA 900
CCCAATGTTC AGCTCACTGG ATATCGAGTG CGGGTGACCC CCAAGGAGAA GACCGGACCA 960
ATGAAAGAAA TCAACCTTGC TCCTGACAGC TCATCCGTGG TTGTATCAGG ACTTATGGTG 1020
GCCACCAAAT ATGAAGTGAG TGTCTATGCT CTTAAGGACA CTTTGACAAG CAGACCAGCT 1080
CAGGGTGTG TCAACCACTCT GGAGAATGTC AGCCACCAA GAAGGGCTCG TGTGACAGAT 1140

GCTACTGAGA CCACCATCAC CATTAGCTGG AGAACCAAGA CTGAGACGAT CACTGGCTTC 1200
CAAGTTGATG CCGTTCCAGC CAATGGCCAG ACTCCAATCC AGAGAACCAT CAAGCCAGAT 1260
GTCAGAAGCT ACACCATCAC AGGTTTACAA CCAGGCACTG ACTACAAGAT CTACCTGTAC 1320
ACCTTGAATG ACAATGCTCG GAGCTCCCCT GTGGTCATCG ACGCCTCCAC TGCCATTGAT 1380
5 GCACCATCCA ACCTGCGTTT CCTGGCCACC ACACCCAATT CTTGCTGGT ATCATGGCAG 1440
CCGCCACGTG CCAGGATTAC CGGCTACATC ATCAAGTATG AGAAGCCTGG GTCTCCTCCC 1500
AGAGAAGTGG TCCCTCGGCC CCGCCTGGT GTCACAGAGG CTACTATTAC TGGCCTGGAA 1560
CCGGGAACCG AATATACAAT TTATGTCATT GCCCTGAAGA ATAATCAGAA GAGCGAGCCC 1620
CTGATTGGAA GGAAAAAGAC TAGCGACGAG CTTCCCAAC TGGTAACCCT TCCACACCCC 1680
10 AATCTTCATG GACCAGAGAT CTTGGATGTT CCTTCCACTA GT 1722

SEQ. ID No. 34

LENGTH: 412

TYPE: amino acid

STRANDEDNESS: single

15 TOPOLOGY: linear

MOLECULAR TYPE: peptide

SEQUENCE:

Met Ser Pro Ile Leu Gly Tyr Trp Lys Ile Lys Gly Leu Val Gln

5

10

15

20 Pro Thr Arg Leu Leu Leu Glu Tyr Leu Glu Glu Lys Tyr Glu Glu

20

25

30

His Leu Tyr Glu Arg Asp Glu Gly Asp Lys Trp Arg Asn Lys Lys

35

40

45

Phe Glu Leu Gly Leu Glu Phe Pro Asn Leu Pro Tyr Tyr Ile Asp

	50	55	60
	Gly Asp Val Lys Leu Thr Gln Ser Met Ala Ile Ile Arg Tyr Ile		
	65	70	75
	Ala Asp Lys His Asn Met Leu Gly Gly Cys Pro Lys Glu Arg Ala		
5	80	85	90
	Glu Ile Ser Met Leu Glu Gly Ala Val Leu Asp Ile Arg Tyr Gly		
	95	100	105
	Val Ser Arg Ile Ala Tyr Ser Lys Asp Phe Glu Thr Leu Lys Val		
	110	115	120
10	Asp Phe Leu Ser Lys Leu Pro Glu Met Leu Lys Met Phe Glu Asp		
	125	130	135
	Arg Leu Cys His Lys Thr Tyr Leu Asn Gly Asp His Val Thr His		
	140	145	150
	Pro Asp Phe Met Leu Tyr Asp Ala Leu Asp Val Val Leu Tyr Met		
	155	160	165
15	Asp Pro Met Cys Leu Asp Ala Phe Pro Lys Leu Val Cys Phe Lys		
	170	175	180
	Lys Arg Ile Glu Ala Ile Pro Gln Ile Asp Lys Tyr Leu Lys Ser		
	185	190	195
20	Ser Lys Tyr Ile Ala Trp Pro Leu Gln Gly Trp Gln Ala Thr Phe		
	200	205	210
	Gly Gly Gly Asp His Pro Pro Lys Ser Asp Leu Ile Glu Gly Arg		
	215	220	225
	Gly Ile Pro Arg Asn Ser Gly Ala Pro Pro Arg Leu Ile Cys Asp		
25	230	235	240

5
10
15
20

SEQ. ID No. 35

LENGTH: 24

TYPE: nucleic acid

STRANDEDNESS: single

5 TOPOLOGY: linear

MOLECULAR TYPE: other nucleic acid (synthetic DNA)

SEQUENCE:

GCTCCCTCTG GGCCTCCCAG TCCT

24

SEQ. ID No. 36

10 LENGTH: 24

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULAR TYPE: other nucleic acid (synthetic DNA)

15 SEQUENCE:

GTTGGTGAGG GAGGTGTTGG ATAT

24

SEQ. ID No. 37

LENGTH: 33

TYPE: nucleic acid

20 STRANDEDNESS: single

TOPOLOGY: linear

MOLECULAR TYPE: other nucleic acid (synthetic DNA)

SEQUENCE:

GGCCTCCCGA ATTCGGGTGC CCCACCACGC CTC

33

SEQ. ID No. 38

LENGTH: 33

TYPE: nucleic acid

5 STRANDEDNESS: single

TOPOLOGY: linear

MOLECULAR TYPE: other nucleic acid (synthetic DNA)

SEQUENCE:

CCCACGTGGA TCCATGGCTA ATCTGTCCCC TGT

33

SEQ. ID No. 39

LENGTH: 1239

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

15 MOLECULAR TYPE: other nucleic acid (DNA encoding an artificial polypeptide)

SEQUENCE:

ATGTCCCCTA TACTAGGTTA TTGGAATAATT AAGGGCCTTG TGCAACCCAC TCGACTTCTT 60

TTGGAATATC TTGAAGAAAA ATATGAAGAG CATTTGTATG AGCGCGATGA AGGTGATAAA 120

20 TGGCGAAACA AAAAGTTTGA ATTGGGTTTG GAGTTTCCCA ATCTTCCTTA TTATATTGAT 180

GGTGATGTTA AATTAACACA GTCTATGGCC ATCATACGTT ATATAGCTGA CAAGCACAAC 240

ATGTTGGGTG GTTGTCAAA AGAGCGTGCA GAGATTTCAG TGCTTGAAGG AGCGGTTTTG 300

GATATTAGAT ACGGTGTTTC GAGAATTGCA TATAGTAAAG ACTTTGAAAC TCTCAAAGTT 360

GATTTTCTTA GCAAGCTACC TGAAATGCTG AAAATGTTTCG AAGATCGTTT ATGTCATAAA 420
ACATATTTAA ATGGTGATCA TGTAACCCAT CCTGACTTCA TGTGTATGA CGCTCTTGAT 480
GTTGTTTAT ACATGGACCC AATGTGCCTG GATGCGTTCC CAAAATTAGT TTGTTTAAA 540
AAACGTATTG AAGCTATCCC ACAAATTGAT AAGTACTTGA AATCCAGCAA GTATATAGCA 600
5 TGGCCTTGC AGGGCTGGCA AGCCACGTTT GGTGGTGGCG ACCATCCTCC AAAATCGGAT 660
CTGATCGAAG GTCGTGGGAT CCCAGGAAT TCCGGTGCCC CACCACGCCT CATCTGTGAC 720
AGCCGAGTCC TGCAGAGGTA CCTCTTGGAG GCCAAGGAGG CCGAGAATAT CACGACGGGC 780
TGTGCTGAAC ACTGCAGCTT GAATGAGAAT ATCACTGTCC CAGACACCAA AGTTAATTTT 840
TATGCCGTGA AGAGGATGGA GGTGCGGCAG CAGGCCGTAG AAGTCTGGCA GGCCTGGCC 900
10 CTGCTGTCGG AAGCTGTCCT GCGGGGCCAG GCCCTGTTGG TCAACTCTTCC CCAGCCGTGG 960
GAGCCCTTGC AGCTGCATGT GGATAAAGCC GTCAGTGGCC TTCGCAGCCT CACCACTCTG 1020
CTTCGGGCTC TGGGAGCCCA GAAGGAAGCC ATCTCCCCTC CAGATGCGGC CTCAGCTGCT 1080
CCACTCCGAA CAATCACTGC TGACACTTTC CGAAACTCT TCCGAGTCTA CTCCAATTTT 1140
CTCCGGGGAA AGCTGAAGCT GTACACAGGG GAGGCCTGCA GGACAGGGGA CAGATTAGCC 1200
15 ATGGATCCTC TAGAGTCGAC TCGAGCGGCC GCATCGTGA 1239